SEQUENCE LISTING

<110> Schwab, M.
       Chen, M.

<120> NUCLEOTIDE AND PROTEIN SEQUENCES OF NOGO
       GENES AND METHODS BASED THEREON

<130> 10200-003-999

<140> 09/830,972
<141> 2001-09-24

<150> PCT/US99/26160
<151> 1999-11-05

<150> 60/107,446
<151> 1998-11-06

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cggctcggct cggcacgact cggcctgcct ggcccctgcc agtcttgccc aaccccaca   180
accgcccgcg actctgagga gaagcggccc tgcggcggct gtagctgcag catcgtcggc   240
gacccgccag cc atg gaa gac ata gac cag tcg tcg ctg gtc tcc tcg tcc   291
              Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser
              1   5   10

acg gac agc ccg ccc cgg cct ccg ccc gcc ttc aag tac cag ttc gtg   339
Thr Asp Ser Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val
    15   20   25

acg gag ccc gag gac gag gag gac gag gag gag gag gag gac gag gag   387
Thr Glu Pro Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu
 30   35   40   45

gag gac gac gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc   435
Glu Asp Asp Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro
                50   55   60

gca gcc ggg ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcg ccg   483
Ala Ala Gly Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro
                65   70   75

ctg ctg gac ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg   531
Leu Leu Asp Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro
        80   85   90

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ctg ccg gcc gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa        579
Leu Pro Ala Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu
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cgc agc ccc gcg gcg ccc gcg cca tcc ctg ccg ccc gct gcc gca gtc        627
Arg Ser Pro Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val
110             115             120                 125

ctg ccc tcc aag ctc cca gag gac gac gag cct ccg gcg agg ccc ccg        675
Leu Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
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cct ccg ccg cca gcc ggc gcg agc ccc ctg gcg gag ccc gcc gcg ccc        723
Pro Pro Pro Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro
            145             150             155

cct tcc acg ccg gcc gcg ccc aag cgc agg ggc tcc ggc tca gtg gat        771
Pro Ser Thr Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp
        160             165             170

gag acc ctt ttt gct ctt cct gct gca tct gag cct gtg ata ccc tcc        819
Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser
        175             180             185

tct gca gaa aaa att atg gat ttg atg gag cag cca ggt aac act gtt        867
Ser Ala Glu Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val
190             195             200             205

tcg tct ggt caa gag gat ttc cca tct gtc ctg ctt gaa act gct gcc        915
Ser Ser Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala
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tct ctt cct tct cta tct cct ctc tca act gtt tct ttt aaa gaa cat        963
Ser Leu Pro Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His
            225             230             235

gga tac ctt ggt aac tta tca gca gtg tca tcc tca gaa gga aca att       1011
Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile
        240             245             250

gaa gaa act tta aat gaa gct tct aaa gag ttg cca gag agg gca aca       1059
Glu Glu Thr Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr
        255             260             265

aat cca ttt gta aat aga gat tta gca gaa ttt tca gaa tta gaa tat       1107
Asn Pro Phe Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr
270             275             280             285

tca gaa atg gga tca tct ttt aaa ggc tcc cca aaa gga gag tca gcc       1155
Ser Glu Met Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala
            290             295             300

ata tta gta gaa aac act aag gaa gaa gta att gtg agg agt aaa gac       1203
Ile Leu Val Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp
            305             310             315

aaa gag gat tta gtt tgt agt gca gcc ctt cac agt cca caa gaa tca       1251
Lys Glu Asp Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser
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cct gtg ggt aaa gaa gac aga gtt gtg tct cca gaa aag aca atg gac       1299
Pro Val Gly Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp
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att ttt aat gaa atg cag atg tca gta gta gca cct gtg agg gaa gag    1347
Ile Phe Asn Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu
350             355             360             365

tat gca gac ttt aag cca ttt gaa caa gca tgg gaa gtg aaa gat act    1395
Tyr Ala Asp Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr
            370             375             380

tat gag gga agt agg gat gtg ctg gct gct aga gct aat gtg gaa agt    1443
Tyr Glu Gly Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser
        385             390  ·          395

aaa gtg gac aga aaa tgc ttg gaa gat agc ctg gag caa aaa agt ctt    1491
Lys Val Asp Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu
        400             405             410

ggg aag gat agt gaa ggc aga aat gag gat gct tct ttc ccc agt acc    1539
Gly Lys Asp Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr
    415             420             425

cca gaa cct gtg aag gac agc tcc aga gca tat att acc tgt gct tcc    1587
Pro Glu Pro Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser
430             435             440             445

ttt acc tca gca acc gaa agc acc aca gca aac act ttc cct ttg tta    1635
Phe Thr Ser Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu
            450             455             460

gaa gat cat act tca gaa aat aaa aca gat gaa aaa aaa ata gaa gaa    1683
Glu Asp His Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu
            465             470             475

agg aag gcc caa att ata aca gag aag act agc ccc aaa acg tca aat    1731
Arg Lys Ala Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn
        480             485             490

cct ttc ctt gta gca gta cag gat tct gag gca gat tat gtt aca aca    1779
Pro Phe Leu Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr
        495             500             505

gat acc tta tca aag gtg act gag gca gca gtg tca aac atg cct gaa    1827
Asp Thr Leu Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu
510             515             520             525

ggt ctg acg cca gat tta gtt cag gaa gca tgt gaa agt gaa ctg aat    1875
Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn
            530             535             540

gaa gcc aca ggt aca aag att gct tat gaa aca aaa gtg gac ttg gtc    1923
Glu Ala Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val
            545             550             555

caa aca tca gaa gct ata caa gaa tca ctt tac ccc aca gca cag ctt    1971
Gln Thr Ser Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu
            560             565             570

tgc cca tca ttt gag gaa gct gaa gca act ccg tca cca gtt ttg cct    2019
Cys Pro Ser Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro
    575             580             585

gat att gtt atg gaa gca cca tta aat tct ctc ctt cca agc gct ggt    2067
Asp Ile Val Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly
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gct tct gta gtg cag ccc agt gta tcc cca ctg gaa gca cct cct cca        2115
Ala Ser Val Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro
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gtt agt tat gac agt ata aag ctt gag cct gaa aac ccc cca cca tat        2163
Val Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr
            625                     630                 635

gaa gaa gcc atg aat gta gca cta aaa gct ttg gga aca aag gaa gga        2211
Glu Glu Ala Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly
            640                     645                 650

ata aaa gag cct gaa agt ttt aat gca gct gtt cag gaa aca gaa gct        2259
Ile Lys Glu Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala
            655                     660                 665

cct tat ata tcc att gcg tgt gat tta att aaa gaa aca aag ctc tcc        2307
Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser
670                     675                 680                 685

act gag cca agt cca gat ttc tct aat tat tca gaa ata gca aaa ttc        2355
Thr Glu Pro Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe
            690                     695                 700

gag aag tcg gtg ccc gaa cac gct gag cta gtg gag gat tcc tca cct        2403
Glu Lys Ser Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro
            705                     710                 715

gaa tct gaa cca gtt gac tta ttt agt gat gat tcg att cct gaa gtc        2451
Glu Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val
            720                     725                 730

cca caa aca caa gag gag gct gtg atg ctc atg aag gag agt ctc act        2499
Pro Gln Thr Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr
            735                     740                 745

gaa gtg tct gag aca gta gcc cag cac aaa gag gag aga ctt agt gcc        2547
Glu Val Ser Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala
750                     755                 760                 765

tca cct cag gag cta gga aag cca tat tta gag tct ttt cag ccc aat        2595
Ser Pro Gln Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn
            770                     775                 780

tta cat agt aca aaa gat gct gca tct aat gac att cca aca ttg acc        2643
Leu His Ser Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr
            785                     790                 795

aaa aag gag aaa att tct ttg caa atg gaa gag ttt aat act gca att        2691
Lys Lys Glu Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile
            800                     805                 810

tat tca aat gat gac tta ctt tct tct aag gaa gac aaa ata aaa gaa        2739
Tyr Ser Asn Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu
            815                     820                 825

agt gaa aca ttt tca gat tca tct ccg att gag ata ata gat gaa ttt        2787
Ser Glu Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe
830                     835                 840                 845
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ccc acg ttt gtc agt gct aaa gat gat tct cct aaa tta gcc aag gag      2835
Pro Thr Phe Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu
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tac act gat cta gaa gta tcc gac aaa agt gaa att gct aat atc caa      2883
Tyr Thr Asp Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln
            865                 870                 875

agc ggg gca gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct      2931
Ser Gly Ala Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser
            880                 885                 890

ttc aag aat ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc      2979
Phe Lys Asn Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe
    895                 900                 905

tcc gaa aat agg tcc agt gta tct aag gca tcc ata tcg cct tca aat      3027
Ser Glu Asn Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn
910                 915                 920                 925

gtc tct gct ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc      3075
Val Ser Ala Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser
            930                 935                 940

aaa tca ctt acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag      3123
Lys Ser Leu Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu
            945                 950                 955

aaa gag gac aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa      3171
Lys Glu Asp Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys
            960                 965                 970

act tca gtt gtt gac ctc ctc tac tgg aga gac att aag aag act gga      3219
Thr Ser Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly
    975                 980                 985

gtg gtg ttt ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc      3267
Val Val Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe
 990                 995                 1000                1005

agc att gtc agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg      3315
Ser Ile Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val
            1010                1015                1020

act atc agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa      3363
Thr Ile Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys
            1025                1030                1035

tca gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct      3411
Ser Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala
            1040                1045                1050

ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt cat      3459
Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His
    1055                1060                1065

gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt gat gat      3507
Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp
1070                1075                1080                1085

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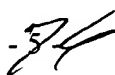
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Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile
            1105                1110                1115

tca ctc ttc agt att cct gtt att tat gaa cgg cat cag gtg cag ata      3651
Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile
            1120                1125                1130

gat cat tat cta gga ctt gca aac aag agt gtt aag gat gcc atg gcc      3699
Asp His Tyr Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala
            1135                1140                1145

aaa atc caa gca aaa atc cct gga ttg aag cgc aaa gca gat           3741
Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
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<213> Rattus sp.

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            20                  25                  30
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        35                  40                  45
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
        50                  55                  60
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65                  70                  75                  80
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
                85                  90                  95
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
            100                 105                 110
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
        115                 120                 125
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
        130                 135                 140
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145                 150                 155                 160
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
                165                 170                 175
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
            180                 185                 190
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
        195                 200                 205
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
        210                 215                 220
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225                 230                 235                 240
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
                245                 250                 255
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
            260                 265                 270
Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
        275                 280                 285
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
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      290                     295                     300
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305                     310                     315                     320
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
                325                     330                     335
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
                340                     345                     350
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
                355                     360                     365
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
370                     375                     380
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385                     390                     395                     400
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
                405                     410                     415
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
                420                     425                     430
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
                435                     440                     445
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
                450                     455                     460
Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465                     470                     475                     480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
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Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
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Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
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Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
                530                     535                     540
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545                     550                     555                     560
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
                565                     570                     575
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
                580                     585                     590
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
                595                     600                     605
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
                610                     615                     620
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625          .          . 630                     635                     640
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
                645                     650                     655
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
                660                     665                     670
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
                675                     680                     685
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
                690                     695                     700
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705                     710                     715                     720
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
                725                     730                     735
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
                740                     745                     750
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
                755                     760                     765
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
   .            770                     775                     780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
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785                    790                   795                    800
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
                       805                   810                    815
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
                  820                   825                    830
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
                  835                   840                    845
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
             850                   855                   860
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865                   870                   875                    880
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
                  885                   890                   895
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
                  900                   905                   910
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
             915                   920                   925
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
        930                   935                   940
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945                   950                   955                    960
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
                  965                   970                   975
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
                  980                   985                   990
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
             995                   1000                  1005
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
        1010                  1015                  1020
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu
1025                  1030                  1035                   1040
Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu
                  1045                  1050                  1055
Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser
             1060                  1065                  1070
Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp
        1075                  1080                  1085
Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala
        1090                  1095                  1100
Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe
1105                  1110                  1115                   1120
Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr
                  1125                  1130                  1135
Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln
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Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
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1               5                   10


        <210> 5
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        <212> PRT
        <213> Bos sp.


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        <222> (2)...(2)
        <223> Xaa = any amino acid


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1               5                   10                  15


        <210> 6
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Lys Xaa Phe Glu Xaa Val Trp Glu Val
1               5


        <210> 7
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        <213> Bos sp.


        <400> 7
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys
1               5                   10


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        <213> Bos sp.


        <400> 8
Lys Ala Val Ala Ala Glu Ala Ser Met Arg Glu Glu Tyr Ala Asp Phe
1               5                   10                  15


        <210> 9
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Glu Tyr Leu Gly Asp Leu Pro Ala Val Leu Pro Thr Glu
1               5                   10


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        <212> PRT
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      <213> Bos sp.

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Glu Ile Ala Asp Ile Gln Asp Gly Ala Gly Ser Leu
1               5               10

      <210> 11
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      <213> Bos sp.

      <400> 11
Lys Pro Tyr Leu Glu Ser Phe Gln Pro Ser Leu Gly Ile Thr Lys
1               5               10              15

      <210> 12
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      <400> 12
Lys Pro Phe Glu Arg Val Trp Glu Val
1               5

      <210> 13
      <211> 11
      <212> PRT
      <213> Bos sp.

      <400> 13
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys
1               5               10

      <210> 14
      <211> 16
      <212> PRT
      <213> Bos sp.

      <400> 14
Lys Gly Val Ala Ala Glu Ala Ser Met Gly Glu Glu Tyr Ala Asp Phe
1               5               10              15

      <210> 15
      <211> 13
      <212> PRT
      <213> Rattus sp.

      <400> 15
Gly Tyr Leu Gly Asn Leu Ser Ala Val Ser Ser Ser Glu
1               5               10

      <210> 16
      <211> 12
      <212> PRT
      <213> Rattus sp.

      <400> 16
Glu Ile Ala Asn Ile Gln Ser Gly Ala Asp Ser Leu
1               5               10

      <210> 17
      <211> 15
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        <212> PRT
        <213> Rattus sp.

        <400> 17
Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser Thr Lys
1               5                   10                  15


        <210> 18
        <211> 9
        <212> PRT
        <213> Rattus sp.

        <400> 18
Lys Pro Phe Glu Gln Ala Trp Glu Val
1               5


        <210> 19
        <211> 11
        <212> PRT
        <213> Rattus sp.

        <400> 19
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys
1               5                   10


        <210> 20
        <211> 16
        <212> PRT
        <213> Rattus sp.

        <400> 20
Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp Phe
1               5                   10                  15


        <210> 21
        <211> 186
        <212> PRT
        <213> Homo sapiens

        <400> 21
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly
1               5                   10                  15
Ser Phe Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser
            20                  25                  30
Val Val Ala Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe
            35                  40                  45
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
    50                  55                  60
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu
65                  70                  75                  80
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Phe Tyr Val Asn Ser Thr
                85                  90                  95
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
            100                 105                 110
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
        115                 120                 125
Phe Asn Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr
        130                 135                 140
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Ile Asp Gln Tyr Leu
145                 150                 155                 160
Gly Leu Val Arg Thr His Ile Asn Ala Val Val Ala Lys Ile Gln Ala
                165                 170                 175
```

```
Lys Ile Pro Gly Ala Lys Arg His Ala Glu
            180                 185


        <210> 22
        <211> 186
        <212> PRT
        <213> Rattus sp.


        <400> 22
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly
  1               5                  10                  15
Ser Phe Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser
            20                  25                  30
Val Val Ala Tyr Leu Ala Leu Ala Ala Leu Ser Ala Thr Ile Ser Phe
            35                  40                  45
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
    50                  55                  60
His Pro Phe Lys Ala Tyr Leu Glu Leu Glu Ile Thr Leu Ser Gln Glu
65                  70                  75                  80
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr
                85                  90                  95
Leu Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
            100                 105                 110
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
            115                 120                 125
Phe Asn Gly Leu Thr Leu Leu Leu Met Ala Val Val Ser Met Phe Thr
    130                 135                 140
Leu Pro Val Val Tyr Val Lys His Gln Ala Gln Val Asp Gln Tyr Leu
145                 150                 155                 160
Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala
                165                 170                 175
Lys Ile Pro Gly Ala Lys Arg His Ala Glu
            180                 185


        <210> 23
        <211> 186
        <212> PRT
        <213> Gallus gallus


        <400> 23
Asn Leu Leu Tyr Trp Arg Asp Ile Lys Gln Thr Gly Ile Val Phe Gly
  1               5                  10                  15
Ser Leu Leu Leu Leu Leu Phe Ser Leu Thr Gln Phe Ser Val Val Ser
            20                  25                  30
Val Val Ala Tyr Leu Ala Leu Ala Gly Leu Ser Ala Thr Ile Ser Phe
            35                  40                  45
Arg Ile Tyr Lys Ser Val Leu Gln Ala Val Gln Lys Thr Asp Glu Gly
    50                  55                  60
His Pro Phe Lys Ala Tyr Leu Asp Met Glu Met Asn Leu Ser Gln Asp
65                  70                  75                  80
Gln Ile Gln Lys Tyr Thr Asp Cys Leu Gln Leu Tyr Val Asn Ser Thr
                85                  90                  95
Val Lys Glu Leu Arg Arg Leu Phe Leu Val Gln Asp Leu Val Asp Ser
            100                 105                 110
Leu Lys Phe Ala Val Leu Met Trp Leu Leu Thr Tyr Val Gly Ala Leu
            115                 120                 125
Phe Asn Gly Leu Thr Leu Leu Ile Met Ala Val Val Ser Met Phe Thr
    130                 135                 140
Leu Pro Val Val Tyr Asp Lys Tyr Gln Ala Gln Ile Asp Gln Tyr Leu
145                 150                 155                 160
Gly Leu Val Arg Thr His Ile Asn Thr Val Val Ala Lys Ile Gln Ala
                165                 170                 175
```

```
Lys Ile Pro Gly Ala Lys Arg Lys Ala Glu
            180             185


        <210> 24
        <211> 186
        <212> PRT
        <213> Bos sp.


        <400> 24
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
 1               5               10                  15
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
            20              25                  30
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
        35              40                  45
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
    50              55                  60
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
65              70                  75                  80
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
                85              90                  95
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
            100             105                 110
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu
            115             120                 125
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser
130                 135                 140
Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu
145                 150                 155                 160
Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala
                165             170                 175
Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
            180             185


        <210> 25
        <211> 186
        <212> PRT
        <213> Rattus sp.


        <400> 25
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
 1               5               10                  15
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
            20              25                  30
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
        35              40                  45
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
    50              55                  60
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
65              70                  75                  80
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser Thr
                85              90                  95
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
            100             105                 110
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu
            115             120                 125
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser
130                 135                 140
Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr Leu
145                 150                 155                 160
Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln Ala
                165             170                 175
```

```
Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
            180                 185


        <210> 26
        <211> 194
        <212> PRT
        <213> C. elegans


        <400> 26
Asp Val Ile Tyr Trp Arg Asp Ala Lys Lys Ser Ala Ile Val Leu Ser
 1               5                  10                  15
Leu Ala Leu Leu Val Leu Phe Val Leu Ala Lys Tyr Pro Leu Leu Thr
            20                  25                  30
Val Val Thr Tyr Ser Leu Leu Leu Ala Leu Gly Ala Ala Ala Gly Phe
            35                  40                  45
Arg Val Phe Lys Lys Val Glu Ala Gln Ile Lys Lys Thr Asp Ser Glu
 50                  55                  60
His Pro Phe Ser Glu Ile Leu Ala Gln Asp Leu Thr Leu Pro Gln Glu
 65                  70                  75                  80
Lys Val His Ala Gln Ala Asp Val Phe Val Glu His Ala Thr Cys Ile
            85                  90                  95
Ala Asn Lys Leu Lys Lys Leu Val Phe Val Glu Ser Pro Leu Glu Ser
            100                 105                 110
Ile Lys Phe Gly Leu Val Leu Trp Ser Leu Thr Tyr Ile Ala Ser Trp
            115                 120                 125
Phe Ser Gly Phe Thr Leu Ala Ile Leu Gly Leu Leu Gly Val Phe Ser
            130                 135                 140
Val Pro Lys Val Tyr Glu Ser Asn Gln Glu Ala Ile Asp Pro His Leu
145                 150                 155                 160
Ala Thr Ile Ser Gly His Leu Lys Asn Val Gln Asn Ile Ile Asp Glu
            165                 170                 175
Lys Leu Pro Phe Leu Arg Ser Ala Pro Val Ala Ala Glu Glu Lys Lys
            180                 185                 190
Asp Gln


        <210> 27
        <211> 150
        <212> PRT
        <213> D. melanogaster


        <400> 27
Asn Leu Leu Leu Trp Arg Asn Ser Arg Lys Thr Leu Ile Val Phe Thr
 1               5                  10                  15
Gly Ile Leu Leu Leu Leu Leu Asp Val Met Val His Ser Val Ile Ser
            20                  25                  30
Val Ile Ser Met Val Gly Ile Thr Val Leu Ile Ala Ala Ile Gly His
            35                  40                  45
Arg Leu Leu Val Gln Phe Trp Ser Ile Trp Lys Lys Asp Glu Asn Lys
 50                  55                  60
Asp Gln Ile Leu Arg Phe Tyr Pro His Pro Lys Ile Glu Ile Pro Arg
 65                  70                  75                  80
Glu Glu Thr Leu Tyr Leu Ala Gly Lys Ala Val Ser His Ile Asn Leu
            85                  90                  95
Ile Leu Asn Arg Met Ile Glu Leu Leu Leu Val Glu Lys Trp Glu Asp
            100                 105                 110
Ser Leu Lys Phe Leu Val Leu Leu Cys Gly Ile Asn Leu Leu Gly Asp
            115                 120                 125
Cys Phe Asn Gly Leu Thr Leu Leu Ile Phe Gly Met Cys Ile Cys Cys
            130                 135                 140
Leu Thr Leu Leu Tyr Leu
145                 150
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<210> 28
<211> 3833
<212> DNA
<213> Bos sp.

<400> 28
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gagaaggcaa aaaatccatt tgtagagaga aatttaacag aattttcaga attggaatat    180
tcagaaatgg aatcatcatt cagtggctct caaaaggcag aacctgccgt aacagtagcg    240
aatcctaggg acgaaatagt tgtgaggagt agagataaag aagaggactt agttagtctt    300
aacatccttc atactcagca ggagttatct acagtcctta cgaaatcagt tgaagaagaa    360
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gctgtatttg gggaattgca aagaaagtgg agctgacaga aataacccctt ttcacagttt    3240
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ctaatgcttc caaaaatgtt tgcaaatatc aaacattgtt atgtaagaaa atataaatga    3720
cgatttatac aattgtggtt taagctgtat tgaactaaat ctgtggaatg cattgtgaac    3780
tgtaaaagca aagtatcaat aaagcttata gacttaaaaa aaaaaaaaaa aaa           3833
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<210> 29
<211> 1178
<212> PRT
<213> Homo sapiens

<220>
<221> VARIANT
<222> (1)...(1178) at all Xaa position
<223> Xaa = any amino acid

<400> 29

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1               5                   10                  15
Pro Arg Pro Gln Pro Ala Phe Lys Tyr Gln Phe Val Arg Glu Pro Glu
            20                  25                  30
Asp Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Asp Glu Asp Glu Asp
        35                  40                  45
Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser
    50                  55                  60
Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp
65                  70                  75                  80
Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
                85                  90                  95
Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro
            100                 105                 110
Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val
            115                 120                 125
Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro
    130                 135                 140
Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr
145                 150                 155                 160
Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro
                165                 170                 175
Lys Arg Arg Gly Ser Ser Gly Ala Val Val Xaa Xaa Xaa Xaa Lys Ile
            180                 185                 190
Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly Gln Glu
    195                 200                 205
Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Xaa Pro Ser Leu
210                 215                 220
Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His Glu Tyr Leu Gly Asn
225                 230                 235                 240
Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser
                245                 250                 255
Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp
            260                 265                 270
Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser
    275                 280                 285
Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn
    290                 295                 300
Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp Glu Glu Glu Lys Leu
305                 310                 315                 320
Val Ser Asn Asn Ile Leu His Xaa Gln Gln Glu Leu Pro Thr Ala Leu
                325                 330                 335
```

```
Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys
            340             345             350
Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu
            355             360             365
Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp
    370             375             380
Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser
385             390             395             400
Asn Leu Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu
            405             410             415
Gln Thr Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser
            420             425             430
Phe Pro Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile
            435             440             445
Thr Cys Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn
    450             455             460
Ile Phe Pro Leu Leu Glu Asp Pro Thr Ser Glu Asn Xaa Thr Asp Glu
465             470             475             480
Lys Lys Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr
            485             490             495
Ser Thr Lys Thr Ser Asn Pro Phe Phe Val Ala Ala Gln Asp Ser Glu
            500             505             510
Thr Asp Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val
            515             520             525
Val Ala Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala
    530             535             540
Cys Glu Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu
545             550             555             560
Thr Lys Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu
            565             570             575
Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr
            580             585             590
Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser
            595             600             605
Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro
    610             615             620
Leu Glu Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu
625             630             635             640
Asn Pro Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Val Ser
            645             650             655
Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu
            660             665             670
Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys
            675             680             685
Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser
            690             695             700
Glu Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val
705             710             715             720
Glu Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp
            725             730             735
Ser Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val
            740             745             750
Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu
            755             760             765
Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro Glu Gly Gly Lys Pro Tyr
    770             775             780
Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn Thr Lys Asp Thr Leu Leu
785             790             795             800
Pro Asp Glu Val Ser Thr Leu Ser Lys Lys Glu Lys Ile Pro Leu Gln
            805             810             815
Met Glu Glu Leu Ser Thr Ala Val Tyr Ser Asn Asp Asp Leu Phe Ile
            820             825             830
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Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu Thr Phe Ser Asp Ser Ser
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Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Leu Ile Ser Ser Lys Thr
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Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr Thr Asp Leu Glu Val Ser
865                 870                 875                 880
His Lys Ser Glu Ile Ala Asn Ala Pro Asp Gly Ala Gly Ser Leu Pro
            885                 890                 895
Cys Thr Glu Leu Pro His Asp Leu Ser Leu Lys Asn Ile Gln Pro Lys
        900                 905                 910
Val Glu Glu Lys Ile Ser Phe Ser Asp Asp Phe Ser Lys Asn Gly Ser
        915                 920                 925
Ala Thr Ser Lys Val Leu Leu Leu Pro Pro Asp Val Ser Ala Leu Gly
        930                 935                 940
His Thr Gln Ala Glu Ile Glu Ser Ile Val Lys Pro Lys Val Leu Glu
945                 950                 955                 960
Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp Arg
            965                 970                 975
Ser Pro Ser Ala Ile Phe Ser Ala Asp Leu Gly Lys Thr Ser Val Val
            980                 985                 990
Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe Gly
        995                 1000                1005
Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val Ser
    1010.               1015                1020
Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser Phe
1025                1030                1035                1040
Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu Gly
            1045                1050                1055
His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu Glu
            1060                1065                1070
Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Cys Thr
            1075                1080                1085
Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp Ser
        1090                1095                1100
Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala Leu
1105                1110                1115                1120
Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe Ser
            1125                1130                1135
Val Pro Val Ile Tyr Glu Arg His Gln Ala Gln Ile Asp His Tyr Leu
            1140                1145                1150
Gly Leu Ala Asn Lys Asn Val Lys Asp Ala Met Ala Lys Ile Gln Ala
            1155                1160                1165
Lys Ile Pro Gly Leu Lys Arg Lys Ala Glu
        1170                1175
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        <210> 30
        <211> 1163
        <212> PRT
        <213> Rattus sp.

        <220>
        <221> VARIANT
        <222> (1)...(1163) at all Xaa position
        <223> Xaa = any amino acid

        <400> 30

```
Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser
 1               5                   10                  15
Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro
            20                  25                  30
Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp
        35                  40                  45
```

```
Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly
    50                  55                  60
Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp
65                  70                  75                  80
Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala
                85                  90                  95
Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro
            100                 105                 110
Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser
        115                 120                 125
Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro
    130                 135                 140
Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr
145                 150                 155                 160
Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu
                165                 170                 175
Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu
            180                 185                 190
Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly
    195                 200                 205
Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro
    210                 215                 220
Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu
225                 230                 235                 240
Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr
                245                 250                 255
Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe
            260                 265                 270
Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met
            275                 280                 285
Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val
    290                 295                 300
Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp
305                 310                 315                 320
Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly
                325                 330                 335
Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn
            340                 345                 350
Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp
            355                 360                 365
Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly
    370                 375                 380
Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp
385                 390                 395                 400
Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp
            405                 410                 415
Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro
            420                 425                 430
Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser
    435                 440                 445
Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His
    450                 455                 460
Thr Ser Glu Asn Xaa Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala
465                 470                 475                 480
Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu
                485                 490                 495
Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu
            500                 505                 510
Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr
    515                 520                 525
Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr
    530                 535                 540
```

```
Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser
545                     550                 555                 560
Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser
                565                 570                 575
Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val
                580                 585                 590
Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val
        595                 600                 605
Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr
    610                 615                 620
Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala
625                 630                 635                 640
Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu
                645                 650                 655
Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile
                660                 665                 670
Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro
        675                 680                 685
Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser
    690                 695                 700
Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu
705                 710                 715                 720
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr
                725                 730                 735
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser
                740                 745                 750
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln
        755                 760                 765
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser
    770                 775                 780
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu
785                 790                 795                 800
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn
                805                 810                 815
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr
                820                 825                 830
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe
    835                 840                 845
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp
    850                 855                 860
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala
865                 870                 875                 880
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn
                885                 890                 895
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn
        900                 905                 910
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala
        915                 920                 925
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu
    930                 935                 940
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp
945                 950                 955                 960
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val
                965                 970                 975
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe
        980                 985                 990
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val
        995                 1000                1005
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile Ser
    1010                1015                1020
Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp Glu
1025                1030                1035                1040
```

Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser Glu
              1045   1050   1055
Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn Ser
              1060   1065   1070
Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp Asp Leu Val Asp
          1075   1080   1085
Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe Thr Tyr Val Gly Ala
        1090   1095   1100
Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu Ala Leu Ile Ser Leu Phe
1105   1110   1115   1120
Ser Ile Pro Val Ile Tyr Glu Arg His Gln Val Gln Ile Asp His Tyr
              1125   1130   1135
Leu Gly Leu Ala Asn Lys Ser Val Lys Asp Ala Met Ala Lys Ile Gln
          1140   1145   1150
Ala Lys Ile Pro Gly Leu Lys Arg Lys Ala Asp
        1155   1160

        <210> 31
        <211> 1568
        <212> DNA
        <213> Rattus sp.

        <400> 31
caggcttagt ctggggaagc gggtgtttca tgtctcaggg agaattttgc agtttacagc   60
gtttctgttg gtatgcataa tttgtaattg ctgctggagg gcagatcgtg gcaagaaatg   120
gacggacaga agaaacattg gaaggacaag gttgttgacc tcctctactg gagagacatt   180
aagaagactg gagtggtgtt tggtgccagc ttattcctgc tgctgtctct gacagtgttc   240
agcattgtca gtgtaacggc ctacattgcc ttggccctgc tctcggtgac tatcagcttt   300
aggatatata agggcgtgat ccaggctatc cagaaatcag atgaaggcca cccattcagg   360
gcatatttag aatctgaagt tgctatatca gaggaattgg ttcagaaata cagtaattct   420
gctcttggtc atgtgaacag cacaataaaa gaactgaggc ggcttttctt agttgatgat   480
ttagttgatt ccctgaagtt tgcagtgttg atgtgggtgt ttacttatgt tggtgccttg   540
ttcaatggtc tgacactact gattttagct ctgatctcac tcttcagtat tcctgttatt   600
tatgaacggc atcaggtgca gatagatcat atctaggac ttgcaaacaa gagtgttaag   660
gatgccatgg ccaaaatcca agcaaaaatc cctggattga agcgcaaagc agattgaaaa   720
agccccaaac agaagttcat ctttaaaggg gacactcact tgattacggg ggtgggaggt   780
cagggtgag cccttggtgg ccgtgcggtt tcagctcttt attttagca gtgcactgtt   840
tgaggaaaaa ttacctgtct tgacttcctg tgtttatcat cttaagtatt gtaagctgct   900
gtgtatggat ctcattgtag tcacacttgt cttccccaat gaggcgcctg gtgaataaag   960
gactcgggga aagctgtgca ttgtatctgc tgcagggtag tctagctgta tgcagagagt   1020
tgtaaagaag gcaaatctgg gggcagggaa aacccttttc acagtgtact gtgtttggtc   1080
agtgtaaaac tgatgcagat ttttctgaaa tgaaatgttt agatgagagc atactactaa   1140
agcagagtgg aaaactctgt ctttatggtg tgttctaggt gtattgtgaa tttactgtta   1200
tattgccaat ataagtaaat atagacctaa tctatatata gtgtttcaca aagcttagat   1260
ctttaacctt gcagctgccc cacagtgctt gacctctgag tcattggtta tgcagtgtag   1320
tcccaagcac ataaactagg aagagaaatg tatttgtagg agtgctacct accacctgtt   1380
ttcaagaaaa tatagaactc caacaaaaat atagaatgtc atttcaaaga cttactgtat   1440
gtatagttaa ttttgtcaca gactctgaaa ttctatggac tgaatttcat gcttccaaat   1500
gtttgcagtt atcaaacatt gttatgcaag aaatcataaa atgaagactt ataccattgt   1560
ggtttaag   1568

        <210> 32
        <211> 141
        <212> PRT
        <213> Rattus sp.

        <400> 32
Gln Ala Ser Gly Glu Ala Gly Val Ser Cys Leu Arg Glu Asn Phe Ala
 1   5   10   15
Val Tyr Ser Val Ser Val Gly Met His Asn Leu Leu Leu Leu Glu Gly
              20   25   30
Arg Ser Trp Gln Glu Met Asp Gly Gln Lys Lys His Trp Lys Asp Lys

```
              35                    40                    45
Val Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val
          50                    55                    60
Phe Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile
65                    70                    75                    80
Val Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile
                  85                    90                    95
Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Ala Lys Ser Asp
                  100                   105                   110
Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile Ser
              115                   120                   125
Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly
          130                   135                   140
```

<210> 33
<211> 18
<212> PRT
<213> Bos sp.

<400> 33
```
Ser Tyr Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu
1                   5                     10                    15
Glu Ala
```

<210> 34
<211> 13
<212> DNA
<213> Homo sapiens

<400> 34
```
gccgccrcca tgg                                                          13
```

<210> 35
<211> 248
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (248) at all n positions
<223> n=a, c, g or t

<400> 35
```
gagccgtcac cacagtaggt ccctcggctc agtcggccca gcccctctca gtcctcccca     60
acccccacaa ccgcccgcgc tcctgagacg cgccccggcg gcggcggcan agctgcagca    120
tcatctccac cctccagcca tggaagacct ggaccagtct cctctggtct cgtcctcgga    180
cagcccaccc cggccgcagc ccgcgttcaa gtaccagttc gtgagggagc ccgaggacga    240
ggaggaag                                                             248
```

<210> 36
<211> 379
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)... (36) at all n positions
<223> n=a, c, g or t

<400> 36
```
gaaaatatgg acttgaagga gcagccaggt aacactattt cggctggtca agaggatttc     60
```

```
ccatctgtcc tgcttgaaac tgctgcttct nttccttctc tgtctcctct ctcagccgct      120
tctttcaaag aacatgaata ccttggtaat ttgtcaacag tattacccac tgaaggaaca      180
cttcaagaaa atgtcagtga agcttctaaa gaggtctcag agaaggcaaa aactctactc      240
atagatagag atttaacaga gttttcagaa ttaggaatac tcagaaatgg gatcatcgtt      300
cagtgtctct ccaaaagcag aatctgccgt aaatagtagg caaatcctag gggaagaaat      360
aattcgtgga aaaataaag                                                   379

        <210> 37
        <211> 281
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)... (281) at all n positions
        <223> n=a, c, g or t

        <400> 37
gatagagatt taacagagtt ttcagaatta gaatactcag aaatgggatc atcgttcagt       60
gtctctccaa aagcagaatc tgccgtaata gtagcaaatc ctagggaaga aataatcgtg      120
aaaaataaag atgaagaaga gaagttagtt agtaataaca tccttcatan tcaacaagag      180
ttacctacag ctcttactaa attggttaaa gaggatgaag ttgtgtcttc agaaaaagca      240
aaagacagtt ttatgaaaga gagttgcagt ggaantcctt g                         281

        <210> 38
        <211> 640
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)... (640) at all n positions
        <223> n=a, c, g or t

        <400> 38
ttaaagagga tgaagttgtg tcttcagaaa aagcaaaaga cagttttaat gaaaagagag       60
ttgcagtgga agctcctatg agggaggaat atgcagactt caaaccattt gagcgagtat      120
gggaagtgaa agatagtaag gaagatagtg atatgttggc tgctggaggt aaaatcgaga      180
gcaacttgga aagtaaagtg gataaaaaat gttttgcaga tagccttgag caaactaatc      240
acgaaaaaga tagtgagagt agtaatgatg atacttcttt ccccagtacg ccagaaggta      300
taaaggatcg ttcaggagca tatatcacat gtgctccctt taacccagca gcaactgaga      360
gcattgcaac naacattttt cctttgttgg agatcctact tcagaaaatt agaccgtgaa      420
aaaaaataga agaaagaag gccnaatgtt accgagaaga atactagcac aaanctcaac      480
cctttcttgt gcagcacagg ntctgngaca gatatgtccc acgnttatta ccaagtgctg      540
agantcttgc aacatcctga ngctgactcc gattgttccn gagctttgaa tggattgtgg      600
ttctggtcaa gttntttgan caaatggctt gtcactcgat                           640

        <210> 39
        <211> 346
        <212> DNA
        <213> Homo sapiens

        <220>
        <221> misc_feature
        <222> (1)... (346) at all n positions
        <223> n=a, c, g or t

        <400> 39
ctgtgcccgg ccccacccc tgggcagatg tcccccactg ctaaggctgc tggcttcagg        60
gagggttagc ctgcaccgcc gccaccctgc ccctaagtta ttacctctcc agttcctacc      120
gtactccctg caccgtctca ctgtgtgtnt cgtgtcagta atttatatgg tgttaaaatg      180
tgtatatttt tgtatgtnac tattttnact agggctgagg ggcctgcgcc cagagctggc      240
```

```
ctcccncaac acctgctgcg cttggtaggt gtggtggcgt tatggcagcc cggctgctgc      300
ttggatgcga gnttggnctt gggccggtgc tggggggcac agttgt                    346
```

```
        <210> 40
        <211> 325
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 40
gtggcaaaca tgcctgaagg cctgactcca gatttagtac aggaagcatg tgaaagtgaa       60
ttgaatgaag ttactggtac aaagattgct tatgaaacaa aatggacttg gttcaaacat      120
cagaagttat gcaagagtca ctctatcctg cagcacagct ttgcccatca tttgaagagt      180
cagaagctac tccttcacca gttttgcctg acattgttat ggaagcacca ttgaattctg      240
cagttcctag tgctggtgct tccgtgatac agcccagctc atcaccatta gaggcttctt      300
cagttaatta tgaagcataa acatg                                           325
```

```
        <210> 41
        <211> 338
        <212> DNA
        <213> Homo sapiens
```

```
        <400> 41
gcatgtgaaa gtgaattgaa tgaagttact ggtacaaaga ttgcttatga aacaaaaatg       60
gacttggttc aaacatcaga agttatgcaa gagtcactct atcctgcagc acagctttgc      120
ccatcatttg aagagtcaga agctactcct tcaccagttt tgcctgacat tgttatggaa      180
gcaccattga attctgcagt tcctagtgct ggtgcttccg tgatacagcc cagctcatca      240
ccattagaag cttcttcagt taattatgaa agcataaaac atgagcctga aaaccccccca     300
ccatatgaag aggccatgag tgtatcacta aaaaaagt                             338
```

```
        <210> 42
        <211> 480
        <212> DNA
        <213> Homo sapiens
```

```
        <220>
        <221> misc_feature
        <222> (1)... (480) at all n positions
        <223> n=a, c, g or t
```

```
        <400> 42
aagactggag tggtgtttgg tgccagccta ttcctgctgc tttcattgac agtattcagc       60
attgtgagcg taacagccta cattgccttg ccctgctct ctgtgaccat cagctttagg       120
atatacaagg gtgtgatcca agctatccag aaatcagatg aaggccaccc attcagggca      180
tatctggaat ctgaagttgc tatatctgag gagttggttc agaagtacag taattctgct      240
cttggtcatg tgaactgcac gataaaggaa ctcaggcgcc tcttcttagt tgatgattta      300
gttgattctc tgaagtttgc agtgttgatg tgggtatttta cctatgttgg tgccttgttt     360
aatggtctga cactactgat ttnggctctc attccactcc tncaagtgtt cctggtattt      420
ntgaacggca tcnggcacag ntagatcatt atccaggact tgcaaatagg aatgtaaaga      480
```

```
        <210> 43
        <211> 13
        <212> PRT
        <213> Homo sapiens
```

```
        <400> 43
Met Glu Asp Leu Asp Gln Ser Pro Leu Val Ser Ser Ser
1               5                   10
```

```
        <210> 44
        <211> 16
        <212> PRT
        <213> Homo sapiens
```

<400> 44
Lys Ile Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile Ser Ala Gly
1   5   10   15

<210> 45
<211> 19
<212> PRT
<213> Homo sapiens

<400> 45
Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser Phe Asn
1   5   10   15
Glu Lys Arg

<210> 46
<211> 50
<212> PRT
<213> Homo sapiens

<400> 46
Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu
1   5   10   15
Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val Met Glu Ala
            20   25   30
Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val Ile Gln Pro
        35   40   45
Ser Ser
    50

<210> 47
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 1 sequence

<220>
<221> modified_base
<222> (1)... (26) at all n positions
<223> n=inosine

<400> 47
tcngtnggya anacngcngg yaartc   26

<210> 48
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 1 sequence

<220>
<221> modified_base
<222> (1)... (23) at all n positions
<223> n=inosine

<400> 48

tcngtnggna gnacnggyaa ytc   23

<210> 49
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 1 sequence

<220>
<221> modified_base
<222> (1)... (25) at all n positions
<223> n=inosine

<400> 49
tcngtnggya anacngcggn agrtc   25

<210> 50
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 1 sequence

<220>
<221> modified_base
<222> (1)...(26) at all n positions
<223> n=inosine

<400> 50
tcngtnggna gnacngcngg nagrtc   26

<210> 51
<211> 26
<212> DNA
<213> Artificial Sequence

<220>
<223> degenerate oligonucleotides designed from the bovine NI220
peptide 2 sequence

<220>
<221> modified_base
<222> (1)... (26) at all n positions
<223> n=inosine

<400> 51
garathgcng anathcarga yggnga   26